RAW SEQUENCE LISTING

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Application Serial Number: _____10/524, 983_____

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IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/524,983

DATE: 08/09/2006
TIME: 09:32:12

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Output Set: N:\CRF4\08092006\J524983.raw

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 4 <110> APPLICANT: ALBANG, Richard
 5         FOLKERS, Ulrike
 6         FRITZ, Andreas
 7         GERHARD, Beatrix
 8         HEINRICH, Oliver
 9         ILGENFRITZ, Hilmar
10         MAIER, Dieter
11         SPREAFICO, Fabio
12         WAGNER, Christian
13         DE BOER, Lex
14         MEIMA, Roelf Bernhard
16 <120> TITLE OF INVENTION: NOVEL LIPASES AND USES THEREOF
18 <130> FILE REFERENCE: 246152025100
20 <140> CURRENT APPLICATION NUMBER: US 10/524,983
21 <141> CURRENT FILING DATE: 2005-02-18
23 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/009145
24 <151> PRIOR FILING DATE: 2003-08-15
26 <150> PRIOR APPLICATION NUMBER: EP 02102168.8
27 <151> PRIOR FILING DATE: 2002-08-19
29 <150> PRIOR APPLICATION NUMBER: EP 02102169.6
30 <151> PRIOR FILING DATE: 2002-08-19
32 <150> PRIOR APPLICATION NUMBER: EP 02102170.4
33 <151> PRIOR FILING DATE: 2002-08-19
35 <150> PRIOR APPLICATION NUMBER: EP 02102171.2
36 <151> PRIOR FILING DATE: 2002-08-19
38 <150> PRIOR APPLICATION NUMBER: EP 02102172.0
39 <151> PRIOR FILING DATE: 2002-08-19
41 <150> PRIOR APPLICATION NUMBER: EP 02102173.8
42 <151> PRIOR FILING DATE: 2002-08-19
44 <150> PRIOR APPLICATION NUMBER: EP 02102174.6
45 <151> PRIOR FILING DATE: 2002-08-19
47 <150> PRIOR APPLICATION NUMBER: EP 02102176.1
48 <151> PRIOR FILING DATE: 2002-08-19
50 <150> PRIOR APPLICATION NUMBER: EP 02102178.7
51 <151> PRIOR FILING DATE: 2002-08-19
53 <150> PRIOR APPLICATION NUMBER: EP 02102179.5
54 <151> PRIOR FILING DATE: 2002-08-19
56 <150> PRIOR APPLICATION NUMBER: EP 02102181.1
57 <151> PRIOR FILING DATE: 2002-08-19
59 <150> PRIOR APPLICATION NUMBER: EP 02102183.7
60 <151> PRIOR FILING DATE: 2002-08-19
62 <160> NUMBER OF SEQ ID NOS: 39
64 <170> SOFTWARE: PatentIn version 3.1
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69 <213> ORGANISM: Aspergillus niger
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74 aggtatttaa ctttgggcga taccaactac gcgtgcactt tgaagcatag cacggcgcgc   180
75 cggggatgcg tgtcgtctta tgactataat tgatgtggcc gactgactgc ttggtgttag   240
76 ggatcttgtg tttatcttgg ttttctgtac ttagaagaga gtgccggtgg catggtggtc   300
77 gatataacta gagcaatgcg tgtctccatc ctcatcctca tcggccatcc cttatapccct   360
78 gatggcgccg aagggtgaga atggcgatgg gcgagaataa tatactgtgt atagtctgtc   420
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80 tgctctatat ccgagacaaa ccacaactta ttcaatttaa gcccgagtcc ataatcatcc   540
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82 ttagctcctc actaggacct cccgccgcgt cttggctcct catcaccaac tttccaccta   660
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104 ttggtggtga cccggacaag atcaccatct ggggagaatc agcgtgagat tataccctaa  1980
105 tagcattcga tatacagcgc ctgacatggc acagtggtgc ctacagcgtc ggagcccacc  2040
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114 ccgaagcgat ccagcagttg atgggtgagc ccccccccccc ccccttccc accaatcccc  2580
115 aagatatata tatagtacga gatactaagg tgaaatgaaa atgatagcat ccaaacgctg  2640
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116 ggtcctaaac gaaacccaag ccacgaccct cctatcgcac tatcccaaca tctccgccct   2700
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118 ctacgagtcg atggcgggcg atctgtgcat ggttgctccg aggaggttgc tcagtcagaa   2820
119 gatgaaggag tatgaggagc aagtgtttgc gtatcggtgg gatgtcgctg cgttgaatga   2880
120 ttcgagtacg attggggtgg cgcattttgc tgaggtaatg ccatccatcc atcccctatt   2940
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122 tagatcccgt ttgttttcgc caaccctgtg cagaacatca ctccgttggg aagtgatccc   3060
123 gcaagactgg agttgggtaa tctggccgcg aggatgtgga cggcttttgt gacggatttg   3120
124 gatccgaatg ggcatggtgg tacgttcctc ttctccatct tattagaatt gtgaaatgaa   3180
125 gcgtgtggtt ctaatgaggg tgacagtctc tggtatcccc cactggccga aatacaacct   3240
126 cactgatccg agggactttg tgttccggct accgagggat ggaagttatg tggagaagga   3300
127 tactttagg acggggggga ttgattatat taatacaatt gtgcggtaag ttgctgctaa   3360
128 gtagtactac tatatgtata taggagggtg tgggtgaaaa gtagatagta gtactatatc   3420
129 aaggatggtt agatactata tactatttac tactactgta atgttactat aatcaagact   3480
130 agaagaaagt ctactgattg attacttcga ctgatcgatt gtattgatct agttagtata   3540
131 tcaaatcgac aaagagccgc cgttttttatt cattcatatt tcccgccact aagccagtat   3600
132 actataccat agtagtatag ctggtttagt tgatgccgag cagctcaacc tcgctaattg   3660
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143 <221> NAME/KEY: CDS
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149 1               5                   10                  15
150 gcc tca act cta gac acc agt aat acc cct acc atc aag aga gca gac   96
151 Ala Ser Thr Leu Asp Thr Ser Asn Thr Pro Thr Ile Lys Arg Ala Asp
152             20                  25                  30
153 gca gga aac aac acc tcc tca atc cca aca gcc acc ctc aac aac acc   144
154 Ala Gly Asn Asn Thr Ser Ser Ile Pro Thr Ala Thr Leu Asn Asn Thr
155         35                  40                  45
156 gtc ttc atc ggc cgt tcc ctg ccc gag ttc gag cag gag ttg ttc ctg   192
157 Val Phe Ile Gly Arg Ser Leu Pro Glu Phe Glu Gln Glu Leu Phe Leu
158     50                  55                  60
159 ggt atc aag ttt gct gat gag ccc gtg cga ttc acc ccg tcg acg ttg   240
160 Gly Ile Lys Phe Ala Asp Glu Pro Val Arg Phe Thr Pro Ser Thr Leu
161 65                  70                  75                  80
162 aaa acc gtc tat cgc gcc aat gac agc gac aac ggg gtg tat cat gct   288
163 Lys Thr Val Tyr Arg Ala Asn Asp Ser Asp Asn Gly Val Tyr His Ala
164             85                  90                  95
165 tcc aca gca tcc gga ctg cag act tcc tcg ggg acc gtg ctc tac aac   336
166 Ser Thr Ala Ser Gly Leu Gln Thr Ser Ser Gly Thr Val Leu Tyr Asn
167         100                 105                 110
168 gcc aca gag tat ggg tat gat tgc ccc ggg tat gga tcc gat gag acg   384
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169 Ala Thr Glu Tyr Gly Tyr Asp Cys Pro Gly Tyr Gly Ser Asp Glu Thr
170         115                 120             125
171 gag ctg gcg gag gaa gga tat gcg cgg ttc gat gag aac tgt atg aac        432
172 Glu Leu Ala Glu Glu Gly Tyr Ala Arg Phe Asp Glu Asn Cys Met Asn
173         130                 135             140
174 ctg aat ata att cgg ccc aag aga gag aaa gag gat gag ttg ttg cct        480
175 Leu Asn Ile Ile Arg Pro Lys Arg Glu Lys Glu Asp Glu Leu Leu Pro
176 145                 150             155                 160
177 gtg atg att tgg atc ttt ggt ggt ggt tgg gtg cag ggt gcg act gct        528
178 Val Met Ile Trp Ile Phe Gly Gly Gly Trp Val Gln Gly Ala Thr Ala
179                 165             170                 175
180 gat ccg agg tac aat atg agc tat att gtt cgc cag ggt gcg ttg aat        576
181 Asp Pro Arg Tyr Asn Met Ser Tyr Ile Val Arg Gln Gly Ala Leu Asn
182             180                 185             190
183 gat aag cct gtc ttg ggt gtc tcg atc aat tac cgt gtg gct gcg ttt        624
184 Asp Lys Pro Val Leu Gly Val Ser Ile Asn Tyr Arg Val Ala Ala Phe
185             195                 200             205
186 gga ttc ctt gac tct gtc gag gtt atg gaa tcc ggc aac acg aac cta        672
187 Gly Phe Leu Asp Ser Val Glu Val Met Glu Ser Gly Asn Thr Asn Leu
188         210                 215             220
189 gga ctt cgt gat cag cgc gtc gcc atg cat tgg gtc aaa caa aac atc        720
190 Gly Leu Arg Asp Gln Arg Val Ala Met His Trp Val Lys Gln Asn Ile
191 225                 230             235                 240
192 aag gcg ttt ggt ggt gac ccg gac aag atc acc atc tgg gga gaa tca        768
193 Lys Ala Phe Gly Gly Asp Pro Asp Lys Ile Thr Ile Trp Gly Glu Ser
194                 245             250                 255
195 gct ggt gcc tac agc gtc gga gcc cac ctg gtc acc aac gac ggt gac        816
196 Ala Gly Ala Tyr Ser Val Gly Ala His Leu Val Thr Asn Asp Gly Asp
197             260                 265             270
198 aac gag ggt cta ttc aga gcc gcc atc atg gaa tcc ggc aac gca gtc        864
199 Asn Glu Gly Leu Phe Arg Ala Ala Ile Met Glu Ser Gly Asn Ala Val
200         275                 280             285
201 gga ccc ccc tac aac ggc acg gac tgg tac cag ccg atg tac gac cag        912
202 Gly Pro Pro Tyr Asn Gly Thr Asp Trp Tyr Gln Pro Met Tyr Asp Gln
203         290                 295             300
204 atc gtg aac gca acc aac tgc acc acc tca agc aac acc ctt caa tgc        960
205 Ile Val Asn Ala Thr Asn Cys Thr Thr Ser Ser Asn Thr Leu Gln Cys
206 305                 310             315                 320
207 ctc cgc gaa gtc ccc ttc tca acg atc tac acc gcc gca gac atc ggc       1008
208 Leu Arg Glu Val Pro Phe Ser Thr Ile Tyr Thr Ala Ala Asp Ile Gly
209                 325             330                 335
210 ctg gaa tgg ttc gcc acc atc gac ggc acc ttc atc aaa gaa tat ccc       1056
211 Leu Glu Trp Phe Ala Thr Ile Asp Gly Thr Phe Ile Lys Glu Tyr Pro
212                 340             345                 350
213 caa atc agc att acg gag ggc cgc ttc gcc aag gtc ccc atc ctc cat       1104
214 Gln Ile Ser Ile Thr Glu Gly Arg Phe Ala Lys Val Pro Ile Leu His
215             355                 360             365
216 ggc acc aac acc gac gag ggc gtg agt ttc ggt acg acg ggc gtg aac       1152
217 Gly Thr Asn Thr Asp Glu Gly Val Ser Phe Gly Thr Thr Gly Val Asn
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220  Thr Asp Ala Glu Ala Ile Gln Gln Leu Met Ala Ser Lys Arg Trp Val
221  385                    390                    395                    400
222  cta aac gaa acc caa gcc acg acc ctc cta tcg cac tat ccc aac atc          1248
223  Leu Asn Glu Thr Gln Ala Thr Thr Leu Leu Ser His Tyr Pro Asn Ile
224                         405                    410                    415
225  tcc gcc cta ggc tgt ccc tac gga tgg ggc aac acg acc tgg ccg aag          1296
226  Ser Ala Leu Gly Cys Pro Tyr Gly Trp Gly Asn Thr Thr Trp Pro Lys
227             420                    425                    430
228  ctg ggg tat gaa tat aag cgc tac gag tcg atg gcg ggc gat ctg tgc          1344
229  Leu Gly Tyr Glu Tyr Lys Arg Tyr Glu Ser Met Ala Gly Asp Leu Cys
230             435                    440                    445
231  atg gtt gct ccg agg agg ttg ctc agt cag aag atg aag gag tat gag          1392
232  Met Val Ala Pro Arg Arg Leu Leu Ser Gln Lys Met Lys Glu Tyr Glu
233        450                    455                    460
234  gag caa gtg ttt gcg tat cgg tgg gat gtc gct gcg ttg aat gat tcg          1440
235  Glu Gln Val Phe Ala Tyr Arg Trp Asp Val Ala Ala Leu Asn Asp Ser
236  465                    470                    475                    480
237  agt acg att ggg gtg gcg cat ttt gct gag atc ccg ttt gtt ttc gcc          1488
238  Ser Thr Ile Gly Val Ala His Phe Ala Glu Ile Pro Phe Val Phe Ala
239                         485                    490                    495
240  aac cct gtg cag aac atc act ccg ttg gga agt gat ccc gca aga ctg          1536
241  Asn Pro Val Gln Asn Ile Thr Pro Leu Gly Ser Asp Pro Ala Arg Leu
242             500                    505                    510
243  gag ttg ggt aat ctg gcc gcg agg atg tgg acg gct ttt gtg acg gat          1584
244  Glu Leu Gly Asn Leu Ala Ala Arg Met Trp Thr Ala Phe Val Thr Asp
245             515                    520                    525
246  ttg gat ccg aat ggg cat ggt gtc tct ggt atc ccc cac tgg ccg aaa          1632
247  Leu Asp Pro Asn Gly His Gly Val Ser Gly Ile Pro His Trp Pro Lys
248        530                    535                    540
249  tac aac ctc act gat ccg agg gac ttt gtg ttc cgg cta ccg agg gat          1680
250  Tyr Asn Leu Thr Asp Pro Arg Asp Phe Val Phe Arg Leu Pro Arg Asp
251  545                    550                    555                    560
252  gga agt tat gtg gag aag gat act ttt agg acg ggg ggg att gat tat          1728
253  Gly Ser Tyr Val Glu Lys Asp Thr Phe Arg Thr Gly Gly Ile Asp Tyr
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257             580
260  <210> SEQ ID NO: 3
261  <211> LENGTH: 582
262  <212> TYPE: PRT
263  <213> ORGANISM: Aspergillus niger
265  <400> SEQUENCE: 3
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269             20                    25                   30
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L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date